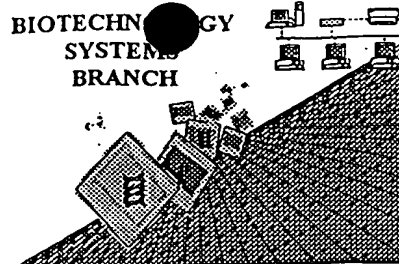
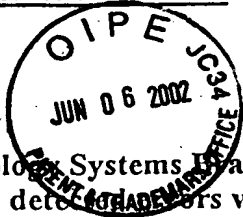


Re-run



RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/647,140

Source: Pt 109

Date Processed by STIC: 6/18/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

*Please mail this Raw Sequence Listing
Error Report with the 905.*

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>
-----------------------	-----------------------------

SERIAL NUMBER: 09/647,140

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | |
|----|---|--|
| 1 | _____ Wrapped Nucleic
_____ Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." |
| 2 | _____ Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. |
| 3 | _____ Misaligned Amino
_____ Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. |
| 4 | _____ Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. |
| 5 | _____ Variable Length | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. |
| 6 | _____ PatentIn 2.0
"bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 7 | _____ Skipped Sequences
(OLD RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |
| 8 | _____ Skipped Sequences
(NEW RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 9 | _____ Use of n's or Xaa's
(NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 10 | _____ Invalid <213>
Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence |
| 11 | _____ Use of <220> | Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) |
| 12 | _____ PatentIn 2.0
"bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. |

AMC – Biotechnology Systems Branch – 06/04/2001



PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/647,140

DATE: 06/18/2001

TIME: 16:26:35

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt

Output Set: N:\CRF3\06182001\I647140.raw

Does Not Comply
Corrected Diskette Needed

P.6

```

3 <110> APPLICANT: Fox Chase Cancer Center
4   Kruh, Gary D.
5   Lee, Kun
6   Belinsky, Martin G.
7   Bain, Lisa J.
9 <120> TITLE OF INVENTION: MRP-Related ABC Transporter Encoding
10  Nucleic Acids and Methods of Use Thereof
12 <130> FILE REFERENCE: FCCC 98-02
14 <140> CURRENT APPLICATION NUMBER: 09/647,140
--> 15 <141> CURRENT FILING DATE: 2001-05-21
17 <150> PRIOR APPLICATION NUMBER: PCT/US99/06644
18 <151> PRIOR FILING DATE: 1999-03-26
20 <150> PRIOR APPLICATION NUMBER: 60/079,759
21 <151> PRIOR FILING DATE: 1998-03-27
23 <150> PRIOR APPLICATION NUMBER: 60/095,153
24 <151> PRIOR FILING DATE: 1998-08-03
26 <160> NUMBER OF SEQ ID NOS: 18
28 <170> SOFTWARE: FastSEQ for Windows Version 3.0
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 4231
33 <212> TYPE: DNA
34 <213> ORGANISM: Homo sapiens
36 <400> SEQUENCE: 1
37  ggacaggcgt ggcgcccgga gccccagcat ccctgcttga ggtccaggag cggagcccgc      60
38  ggccaccgcc gcctgatcag cgcgaccccg gcccgcgccc gcccgccccg gcaagatgct      120
39  gcccggtgtac caggagggtga agcccaaccc gctgcaggac gcgaacatct gctcacgcgt      180
40  gttcttcttg tggtcaatc ccttgtttaa aattggccat aaacggagat tagaggaaga      240
41  tgatatgtat tcagtgtgc cagaagaccg ctcacagcac cttggagagg agttgcaagg      300
42  gttctgggat aaagaagttt taagagctga gaatgacgca cagaagcctt ctttaacaag      360
43  agcaatcata aagtgttact ggaaatctta tttagttttg ggaattttta cgttaattga      420
44  ggaaagtgcc aaagtaatcc agcccatatt tttgggaaaa attattaatt attttgaaaa      480
45  ttatgatccc atggattctg tggttttgaa cacagcgtac gcctatgccg cgggtgtgac      540
46  tttttgcacg ctcatcttgg ctatactgca tcaactatat ttttatcacg ttcagtgtgc      600
47  tgggatgagg ttacgagtag ccatgtgccg tatgatttat cggaaggcac ttcgtcttag      660
48  taacatggcc atggggaaga caaccacagg ccagatagtc aatctgctgt ccaatgatgt      720
49  gaacaagttt gatcaggtga cagtgttctt acacttcctg tgggcaggac cactgcaggc      780
50  gatcgacgtg actgccctac tctggatgga gataggaata tcgtgccttg ctgggatggc      840
51  agttctaata attctcctgc ccttgaaag ctgttttggg aagttgttct catcactgag      900
52  gagtaaaact gcaactttca cggatgccag gatcaggacc atgaatgaag ttataactgg      960
53  tataaggata ataaaaatgt acgcctggga aaagtcattt tcaaacttta ttaccaattt     1020
54  gagaaagaag gagatttcca agattctgag aagttcctgc ctcaggggga tgaatttggc     1080
55  ttcgtttttc agtgcaagca aaatcatcgt gtttgtagacc ttcaccacct acgtgctcct     1140
56  cggcagtggt atcacagcca gccgcgtgtt cgtggcagtg acgctgtatg gggctgtgcg     1200
57  gctgacgggt accctcttct tcccctcagc cattgagagg gtgtcagagg caatcgtcag     1260
58  catccgaaga atccagacct ttttgctact tgatgagata tcacagcgca accgtcagct     1320
59  gccgtcagat ggtaaaaaga tgggtgatgt gcaggatttt actgcttttt gggataaggc     1380
60  atcagagacc ccaactctac aaggcctttc ctttactgtc agacctggcg aattgttagc     1440

```

RAW SEQUENCE LISTING

DATE: 06/18/2001

PATENT APPLICATION: US/09/647,140

TIME: 16:26:35

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt

Output Set: N:\CRF3\06182001\I647140.raw

```

61 tgtgggtcggc cccgtgggag cagggaagtc atcactgtta agtgccgtgc tcggggaatt 1500
62 ggccccaagt caggggctgg tcagcgtgca tggaagaatt gcctatgtgt ctcagcagcc 1560
63 ctgggtgttc tcgggaactc tgaggagtaa ttttttattt gggaagaaat atgaaaagga 1620
64 acgatatgaa aaagtcataa aggcttgtgc tctgaaaaag gatttacagc tgttgaggga 1680
65 tgggtgatctg actgtgatag gagatcgggg aaccacgctg agtggagggc agaaagcacg 1740
66 ggtaaacctt gcaagagcag tgtatcaaga tgctgacatc tatctcctgg acgatcctct 1800
67 cagtgcagta gatgcggaag ttagcagaca cttgttcgaa ctgtgtattt gtcaaatttt 1860
68 gcatgagaag atcacaattt tagtgactca tcagttgcag tacctcaaag ctgcaagtca 1920
69 gattctgata ttgaaagatg gtaaaatggt gcagaagggg acttacactg agttcctaaa 1980
70 atctgggata gattttggct cctttttaa gaaggataat gaggaagtg aacaacctcc 2040
71 agttccagga actccacac taaggaaatcg taccttctca gagtcttcgg tttgggtctca 2100
72 acaatcttct agacctctct tgaaagatgg tgctctggag agccaagata cagagaatgt 2160
73 cccagttaca ctatcagagg agaaccgttc tgaaggaaaa gttgggttttc aggcctataa 2220
74 gaattacttc agagctgggtg ctcactggat tgtcttcatt ttccttattc tcctaaacac 2280
75 tgcagctcag gttgcctatg tgcttcaaga ttgggtggctt tcatactggg caaacaacaa 2340
76 aagtatgcta aatgtcactg taaatggagg aggaaatgta accgagaagc tagatcttaa 2400
77 ctggtaactta ggaattttatt cagggtttaac tgtagctacc gttctttttg gcatagcaag 2460
78 atctctattg gtattctacg tccttggttaa ctcttcacaa actttgcaca acaaaatggt 2520
79 tgagtcatt ctgaaagctc cgggtattatt ctttgataga aatccaatag gaagaatttt 2580
80 aaatcgtttc tccaaagaca ttggacactt ggatgatttg ctgccgctga cgtttttaga 2640
81 tttcatccag acattgctac aagtgggttg tgtggtctct gtggctgtgg ccgtgattcc 2700
82 ttggatcgca atacccttgg tcccccttgg aatcattttc atttttcttc ggcgatattt 2760
83 tttggaaacg tcaagagatg tgaagcgctt ggaatctaca actcggagtc cagtgttttc 2820
84 ccacttgtea tcttctctcc aggggctctg gaccatccgg gcatacaaa cagaagagag 2880
85 gtgtcaggaa ctgtttgatg cacaccagga tttacattca gaggcttggg tcttggtttt 2940
86 gacaacgtcc cgtgtgttcg ccgtccgtct ggatgccatc tgtgccatgt ttgtcatcat 3000
87 cgttgccctt gggctccgta ttctggcaaa aactctggat gccgggcagg ttggtttggc 3060
88 actgtcctat gccctcacgc tcatgggat gtttcagtgg tgtgttcgac aaagtggatga 3120
89 agttgagaat atgatgatct cagtggaaag ggtcattgaa tacacagacc ttgaaaaaga 3180
90 agcaccttgg gaatatcaga aacgcccacc accagcctgg ccccatgaag gagtgataat 3240
91 ctttgacaat gtgaacttca tgtacagtc aggtgggcct ctggtactga agcatctgac 3300
92 agcactcatt aaatcacaa aaaagggttg cattgtggga agaaccggag ctggaaaaag 3360
93 ttccctcatc tcagcccttt ttagattgtc agaaccggaa ggtaaaaatt ggattgataa 3420
94 gatcttgaca actgaaattg gacttcacga ttttaggaag aaaatgtcaa tcatacctca 3480
95 ggaacctgtt ttgttcactg gaacaatgag gaaaaacctg gatcccttta aggagcacac 3540
96 ggatgaggaa ctgtggaatg cttacaaga ggtacaactt aaagaaacca ttgaagatct 3600
97 tcctggtaaa atggatactg aattagcaga atcaggatcc aatttttagt ttggacaaag 3660
98 acaactgggtg tgcccttgcca gggcaattct caggaaaaat cagatattga ttattgatga 3720
99 agcgacggca aatgtggatc caagaactga tgagttaata caaaaaaaaaa tccgggagaa 3780
100 atttgcccac tgcaccgtgc taaccattgc acacagattg aacaccatta ttgacagcga 3840
101 caagataatg gttttagatt caggaagact gaaagaatat gatgagccgt atgttttgct 3900
102 gcaaaaataaa gagagcctat tttacaagat ggtgcaacaa ctgggcaagg cagaagccgc 3960
103 tgccctcact gaaacagcaa aacaggtata cttcaaaaaga aattatccac atattggtca 4020
104 cactgaccac atggttacaa acacttccaa tggacagccc tcgaccttaa ctattttcga 4080
105 gacagcactg tgaatccaac caaaatgtca agtccgttcc gaaggcattt tccactagtt 4140
106 tttggactat gtaaaaccaca ttgtactttt ttttactttg gcaacaaata tttatacata 4200
107 caagatgcta gttcatttga atatttctcc c 4231
110 <210> SEQ ID NO: 2
111 <211> LENGTH: 1325

```

RAW SEQUENCE LISTING

DATE: 06/18/2001

PATENT APPLICATION: US/09/647,140

TIME: 16:26:35

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt

Output Set: N:\CRF3\06182001\I647140.raw

```

112 <212> TYPE: PRT
113 <213> ORGANISM: Homo sapiens
115 <400> SEQUENCE: 2
116 Met Leu Pro Val Tyr Gln Glu Val Lys Pro Asn Pro Leu Gln Asp Ala
117 1 5 10 15
118 Asn Ile Cys Ser Arg Val Phe Phe Trp Trp Leu Asn Pro Leu Phe Lys
119 20 25 30
120 Ile Gly His Lys Arg Arg Leu Glu Glu Asp Asp Met Tyr Ser Val Leu
121 35 40 45
122 Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu Leu Gln Gly Phe Trp
123 50 55 60
124 Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala Gln Lys Pro Ser Leu
125 65 70 75 80
127 Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser Tyr Leu Val Leu Gly
128 85 90 95
129 Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val Ile Gln Pro Ile Phe
130 100 105 110
131 Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr Asp Pro Met Asp Ser
132 115 120 125
133 Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr Val Leu Thr Phe Cys
134 130 135 140
135 Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr Phe Tyr His Val Gln
136 145 150 155 160
137 Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys His Met Ile Tyr Arg
138 165 170 175
139 Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly Lys Thr Thr Thr Gly
140 180 185 190
141 Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn Lys Phe Asp Gln Val
142 195 200 205
143 Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro Leu Gln Ala Ile Ala
144 210 215 220
145 Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile Ser Cys Leu Ala Gly
146 225 230 235 240
147 Met Ala Val Leu Ile Leu Leu Pro Leu Gln Ser Cys Phe Gly Lys
148 245 250 255
149 Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr Phe Thr Asp Ala Arg
150 260 265 270
151 Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile Arg Ile Ile Lys Met
152 275 280 285
153 Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile Thr Asn Leu Arg Lys
154 290 295 300
155 Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys Leu Arg Gly Met Asn
156 305 310 315 320
157 Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile Val Phe Val Thr Phe
158 325 330 335
159 Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr Ala Ser Arg Val Phe
160 340 345 350
161 Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu Thr Val Thr Leu Phe
162 355 360 365

```

RAW SEQUENCE LISTING

DATE: 06/18/2001

PATENT APPLICATION: US/09/647,140

TIME: 16:26:35

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt

Output Set: N:\CRF3\06182001\I647140.raw

```

163 Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg
164      370      375      380
165 Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg
166 385      390      395      400
167 Gln Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr
168      405      410      415
169 Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser
170      420      425      430
171 Phe Thr Val Arg Pro Gly Glu Leu Ala Val Val Gly Pro Val Gly
172      435      440      445
173 Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro
174      450      455      460
175 Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln
176 465      470      475      480
177 Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly
178      485      490      495
179 Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala
180      500      505      510
181 Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile
182      515      520      525
183 Gly Asp Arg Gly Thr Pro Leu Ser Gly Gly Gln Lys Ala Arg Val Asn
184      530      535      540
185 Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp
186 545      550      555      560
187 Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu
188      565      570      575
190 Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His
191      580      585      590
192 Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp
193      595      600      605
194 Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly
195      610      615      620
196 Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln
197 625      630      635      640
198 Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu
199      645      650      655
200 Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly
201      660      665      670
202 Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu
203      675      680      685
204 Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr
205      690      695      700
206 Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Leu
207 705      710      715      720
208 Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp Leu Ser
209      725      730      735
210 Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn Gly Gly
211      740      745      750
212 Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp Tyr Leu Gly Ile Tyr

```

<210> 9
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence source:/note="synthetic construct"

<400> 9
ctdgtgdcg tdgtggg

18

see item 9 on Ena Summary Sheet

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/647,140

DATE: 06/18/2001

TIME: 16:26:36

Input Set : A:\FCCC Kruh ('140) Sequence Listing.txt

Output Set: N:\CRF3\06182001\I647140.raw

15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 1174 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
 1174 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
 1174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
 1259 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
 1259 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
 1259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
 1270 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
 1270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
 1270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 1282 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
 1282 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
 1282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18